



SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: Suerbaum, Sebastian
Labigne, Agnes

(ii) TITLE OF INVENTION: Cloning and Characterization of the flbA
Gene of H. Pylori, Production of Aflagellate Strains

(iii) NUMBER OF SEQUENCES: 13

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
Dunner
(B) STREET: 1300 I Street, N.W.
(C) CITY: Washington
(D) STATE: D.C.
(E) COUNTRY: USA
(F) ZIP: 20005-3315

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/671,757
(B) FILING DATE: 28-JUN-1996
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Meyers, Kenneth J.
(B) REGISTRATION NUMBER: 25,146
(C) REFERENCE/DOCKET NUMBER: 02356.0073-00000

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (202) 408-4000
(B) TELEFAX: (202) 408-4400

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGCCTCGAG GTCGAAAAGC AAGATG

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 27 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GAAATCTTCA TACTGGCAGC TCCAGTC

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGCCAGGAA AGCAAATGGC GATTGATGCG GATTTAAATT CAGGGCTTAT TGATGATAAG	60
GAAGCTAAAA AACGGCGCGC CGCTCTAAGC CAAGAAGCGG ATTTTATGG TGCGATGGAT	120
GGCGCGTCTA AATTT	135

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

CGGGATCCGT GGT TACTAAT GGT TCTAC

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

CGGGATCCTC ATGGCCTCTT CAGAGACC

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2501 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

AGCTTTTTTG TGCCATACTT TTAAACTTTA TATTATAATA AGAGACAAAC ACACCTACCA	60
AAATTAAGGC ATTGATTTTA GATTATGGCA AACGAACGCT CCAAATTAGC TTTTAAAAAG	120
ACTTTCCCTG TCTTTAAACG CTTCTTGCAA TCCAAAGACT TAGCCCTTGT GGTCTTTGTG	180
ATAGCGATTT TAGCGATCAT TATCGTGCCG TTACCGCCTT TTGTGTTGGA TTTTTTACTC	240
ACGATTTCTA TCGCGCTATC GGTGTTGATT ATTTTAATCG GGCTTTATAT TGACAAACCG	300
ACTGATTTTA GCGCTTTCCC CACTTTATTA CTCATTGTAA CCTTATACCG CTTGGCTTTA	360
AATGTCGCCA CCACTAGAAT GATTTTAACC CAAGGCTATA AAGGGCCTAG CGCGGTGAGC	420
ATTATTATCA CGGCGTTTGG GGAATTTAGC GTGAGCGGGA ATTATGTGAT TGGGGCTATT	480
ATCTTTAGTA TTTTAGTGCT GGTGAATTTA TTAGTGGTTA CTAATGGTTC TACTAGGGTT	540
ACTGAAGTTA GGGCGCGATT TGCCCTAGAC GCTATGCCAG GAAAGCAAAT GGCGATTGAT	600
GCGGATTTAA ATTCAGGGCT TATTGATGAT AAGGAAGCTA AAAAACGGCG CGCCGCTCTA	660
AGCCAAGAAG CGGATTTTTA TGGTGCGATG GATGGCGCGT CTAAATTTGT CAAAGGCGAT	720
GCGATCGCTT CTATCATTAT CACGCTTATC AATATCATTG GGGGTTTTTT AGTGGGCGTG	780
TTCCAAAGGG ATATGAGCTT GAGCTTTAGT GCTAGCACTT TCACTATCTT AACCATTGGC	840
GATGGGCTTG TAGGGCAAAT CCCTGCCTTA ATCATTGCGA CACGGACCGG TATTGTCGCC	900
ACTCGCACCA CGCAAAACGA AGAAGAGGAC TTTGCTTCTA AGCTCATCAC ACAGCTCACC	960
AATAAAAGCA AAACTTTAGT GATTGTGGGG GCGATTTATT GCTTTTGCAC CATTCCTGGA	1020

CTCCCTACCT TTTCTTTAGC GTTTGTAGGG GCTCTCTTTT TATTCATCGC ATGGCTGATT	1080
AGCAGGGAGG GAAAGGACGG GTTGCTCACT AAATTAGAAA ATTATTTGAG TCAAAAATTC	1140
GGCTTGATT TGAGCGAAAA ACCCCACAGC TCCAAAATCA AACCCACGC CCCCACCACA	1200
AGGGCTAAAA CCCAAGAAGA GATTAAAAGA GAAGAAGAGC AAGCCATTGA TGAAGTGTTA	1260
AAAATTGAAT TTTTAGAATT GGCTTTAGGC TATCAGCTCT ACAGCTTAGC GGACATGAAA	1320
CAAGGGGGCG ATTTGTTAGA AAGGATTAGG GGTATTAGAA AAAAGATAGC GAGCGATTAT	1380
GGTTTTTTGA TGCCTCAAAT TAGGATTAGG GATAATTTAC AACTCCCCC AACGCATTAT	1440
GAAATCAAGC TTAAGGGCAT TGTGATTGGT GAAGGCATGG TGATGCCGGA TAAGTTTTTA	1500
GCCATGAATA CCGTTTTTGT GAATAAAGAA ATTGAAGGCA TTCCTACTAA AGAGCCGGCT	1560
TTTGGAATGG ACGCTTTATG GATTGAAACT AAAAATAAAG AAGAAGCCAT CATTCAAGGC	1620
TATACCATTA TTGATCCAAG CACCGTTATT GCGACGCACA CCAGCGAATT AGTGAAAAAA	1680
TACGCTGAAG ATTTTATCAC TAAAGATGAA GTGAAATCCC TTTTAGAGCG CTTGGCCAAA	1740
GACTATCCTA CGATTGTAGA AGAGAGTAAA AAAATCCCCA CCGGTGCGAT CCGATCAGTC	1800
TTGCAAGCCT TGTTGCATGA AAAAATCCCC ATTAAAGACA TGCTCACTAT TTTAGAAACG	1860
ATTACCGATA TTGCGCCATT AGTTCAAAC GATGTGAATA TCTTAACCGA ACAAGTGAGG	1920
GCGAGGCTTT CTAGGGTGAT CACTAACGCT TTAAATCTG AAGACGGGCG TTTGAAATTT	1980
TTAACCTTTT CTACCGATAG CGAACAATTT TTGCTTAATA AATTGCGAGA AAATGGCACT	2040
TCTAAGAGCC TACTACTCAA TGTGGGCGAA TTGCAAAAAC TCATTGAAGC GGTCTCTGAA	2100
GAGGCCATGA AAGTCTTGCA AAAAGGGATC GCTCCGGTGA TTTTGATCGT AGAGCCTAAT	2160
TTAAGAAAAG CCCTTTCTAA TCAAATGGAG CAGGCTAGGA TTGATGTAAT CGTGCTAAGC	2220
CATGCTGAAT TAGATCCTAA CTCTAATTTT GAAGCCTTAG GCACGATCCA TATTAACCTT	2280
TAAGGGATAA ATAATTGATA AAAAAGGAGA ATGATGCAAG TTTATCACCT TTCACACATT	2340
GATTTAGACG GCTATGCATG CCAGCTTGTT TCAAACAAT TTTTAAAAA TATCCAATGC	2400
TATAACGCTA ATTACGGGCG TGAAGTCTCA GCGAGAATTT ATGAGATTTT AAACGCGATC	2460
GCTCAATCTA AAGAGAGTGA ATTCCTTATT TTGATTAGCG A	2501

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Ala	Asn	Glu	Arg	Ser	Lys	Leu	Ala	Phe	Lys	Lys	Thr	Phe	Pro	Val
1				5					10					15	
Phe	Lys	Arg	Phe	Leu	Gln	Ser	Lys	Asp	Leu	Ala	Leu	Val	Val	Phe	Val
		20						25					30		
Ile	Ala	Ile	Leu	Ala	Ile	Ile	Ile	Val	Pro	Leu	Pro	Pro	Phe	Val	Leu
		35					40					45			
Asp	Phe	Leu	Leu	Thr	Ile	Ser	Ile	Ala	Leu	Ser	Val	Leu	Ile	Ile	Leu
	50					55					60				
Ile	Gly	Leu	Tyr	Ile	Asp	Lys	Pro	Thr	Asp	Phe	Ser	Ala	Phe	Pro	Thr
65					70					75					80
Leu	Leu	Leu	Ile	Val	Thr	Leu	Tyr	Arg	Leu	Ala	Leu	Asn	Val	Ala	Thr
			85					90						95	
Thr	Arg	Met	Ile	Leu	Thr	Gln	Gly	Tyr	Lys	Gly	Pro	Ser	Ala	Val	Ser
		100						105						110	
Ile	Ile	Ile	Thr	Ala	Phe	Gly	Glu	Phe	Ser	Val	Ser	Gly	Asn	Tyr	Val
		115					120					125			
Ile	Gly	Ala	Ile	Ile	Phe	Ser	Ile	Leu	Val	Leu	Val	Asn	Leu	Leu	Val
	130					135					140				
Val	Thr	Asn	Gly	Ser	Thr	Arg	Val	Thr	Glu	Val	Arg	Ala	Arg	Phe	Ala
145					150					155					160
Leu	Asp	Ala	Met	Pro	Gly	Lys	Gln	Met	Ala	Ile	Asp	Ala	Asp	Leu	Asn
			165					170						175	

Ser Gly Leu Ile Asp Asp Lys Glu Ala Lys Lys Arg Arg Ala Ala Leu
 180 185 190

Ser Gln Glu Ala Asp Phe Tyr Gly Ala Met Asp Gly Ala Ser Lys Phe
 195 200 205

Val Lys Gly Asp Ala Ile Ala Ser Ile Ile Ile Thr Leu Ile Asn Ile
 210 215 220

Ile Gly Gly Phe Leu Val Gly Val Phe Gln Arg Asp Met Ser Leu Ser
 225 230 235 240

Phe Ser Ala Ser Thr Phe Thr Ile Leu Thr Ile Gly Ala Gly Leu Val
 245 250 255

Gly Gln Ile Pro Ala Leu Ile Ile Ala Thr Arg Thr Gly Ile Val Ala
 260 265 270

Thr Arg Thr Thr Gln Asn Glu Glu Glu Asp Phe Ala Ser Lys Leu Ile
 275 280 285

Thr Gln Leu Thr Asn Lys Ser Lys Thr Leu Val Ile Val Gly Ala Ile
 290 295 300

Tyr Cys Phe Cys Thr Ile Pro Gly Leu Pro Thr Phe Ser Leu Ala Phe
 305 310 315 320

Val Gly Ala Leu Phe Leu Phe Ile Ala Trp Leu Ile Ser Arg Glu Gly
 325 330 335

Lys Asp Gly Leu Leu Thr Lys Leu Glu Asn Tyr Leu Ser Gln Lys Phe
 340 345 350

Gly Leu Asp Leu Ser Glu Lys Pro His Ser Ser Lys Ile Lys Pro His
 355 360 365

Ala Pro Thr Thr Arg Ala Lys Thr Gln Glu Glu Ile Lys Arg Glu Glu
 370 375 380

Glu Gln Ala Ile Asp Glu Val Leu Lys Ile Glu Phe Leu Glu Leu Ala
 385 390 395 400

Leu Gly Thr Gln Leu Tyr Ser Leu Ala Asp Met Lys Gln Gly Gly Asp
 405 410 415

Leu Leu Glu Arg Ile Arg Gly Ile Arg Lys Lys Ile Ala Ser Asp Tyr
 420 425 430

Gly	Phe	Leu	Met	Pro	Gln	Ile	Arg	Ile	Arg	Asp	Asn	Leu	Gln	Leu	Pro	435	440	445	
Pro	Thr	His	Tyr	Glu	Ile	Lys	Leu	Lys	Gly	Ile	Val	Ile	Gly	Glu	Gly	450	455	460	
Met	Val	Met	Pro	Asp	Lys	Phe	Leu	Ala	Met	Asn	Thr	Gly	Phe	Val	Asn	465	470	475	480
Lys	Glu	Ile	Glu	Gly	Ile	Pro	Thr	Lys	Glu	Pro	Ala	Phe	Gly	Met	Asp	485	490	495	
Ala	Leu	Trp	Ile	Glu	Thr	Lys	Asn	Lys	Glu	Glu	Ala	Ile	Ile	Gln	Gly	500	505	510	
Tyr	Thr	Ile	Ile	Asp	Pro	Ser	Thr	Val	Ile	Ala	Thr	His	Thr	Ser	Glu	515	520	525	
Leu	Val	Lys	Lys	Tyr	Ala	Glu	Asp	Phe	Ile	Thr	Lys	Asp	Glu	Val	Lys	530	535	540	
Ser	Leu	Leu	Glu	Arg	Leu	Ala	Lys	Asp	Tyr	Pro	Thr	Ile	Val	Glu	Glu	545	550	555	560
Ser	Lys	Lys	Ile	Pro	Thr	Gly	Ala	Ile	Arg	Ser	Val	Leu	Gln	Ala	Leu	565	570	575	
Leu	His	Glu	Lys	Ile	Pro	Ile	Lys	Asp	Met	Leu	Thr	Ile	Leu	Glu	Thr	580	585	590	
Ile	Thr	Asp	Ile	Ala	Pro	Leu	Val	Gln	Asn	Asp	Val	Asn	Ile	Leu	Thr	595	600	605	
Glu	Gln	Val	Arg	Ala	Arg	Leu	Ser	Arg	Val	Ile	Thr	Asn	Ala	Phe	Lys	610	615	620	
Ser	Glu	Asp	Gly	Arg	Leu	Lys	Phe	Leu	Thr	Phe	Ser	Thr	Asp	Ser	Glu	625	630	635	640
Gln	Phe	Leu	Leu	Asn	Lys	Leu	Arg	Glu	Asn	Gly	Thr	Ser	Lys	Ser	Leu	645	650	655	
Leu	Leu	Asn	Val	Gly	Glu	Leu	Gln	Lys	Leu	Ile	Glu	Ala	Val	Ser	Glu	660	665	670	
Glu	Ala	Met	Lys	Val	Leu	Gln	Lys	Gly	Ile	Ala	Pro	Val	Ile	Leu	Ile	675	680	685	

Val Glu Pro Asn Leu Arg Lys Ala Leu Ser Asn Gln Met Glu Gln Ala
690 695 700

Arg Ile Asp Val Ile Val Leu Ser His Ala Glu Leu Asp Pro Asn Ser
705 710 715 720

Asn Phe Glu Ala Leu Gly Thr Ile His Ile Asn Phe
725 730

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 732 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Ala	Asn	Glu	Arg	Ser	Lys	Leu	Ala	Phe	Lys	Lys	Thr	Phe	Pro	Val
1				5					10					15	
Phe	Lys	Arg	Phe	Leu	Gln	Ser	Lys	Asp	Leu	Ala	Leu	Val	Val	Phe	Val
		20						25					30		
Ile	Ala	Ile	Leu	Ala	Ile	Ile	Ile	Val	Pro	Leu	Pro	Pro	Phe	Val	Leu
		35					40					45			
Asp	Phe	Leu	Leu	Thr	Ile	Ser	Ile	Ala	Leu	Ser	Val	Leu	Ile	Ile	Leu
	50					55					60				
Ile	Gly	Leu	Tyr	Ile	Asp	Lys	Pro	Thr	Asp	Phe	Ser	Ala	Phe	Pro	Thr
65					70					75					80
Leu	Leu	Leu	Ile	Val	Thr	Leu	Tyr	Arg	Leu	Ala	Leu	Asn	Val	Ala	Thr
			85					90						95	
Thr	Arg	Met	Ile	Leu	Thr	Gln	Gly	Tyr	Lys	Gly	Pro	Ser	Ala	Val	Ser
		100						105						110	
Ile	Ile	Ile	Thr	Ala	Phe	Gly	Glu	Phe	Ser	Val	Ser	Gly	Asn	Tyr	Val
		115					120					125			
Ile	Gly	Ala	Ile	Ile	Phe	Ser	Ile	Leu	Val	Leu	Val	Asn	Leu	Leu	Val
	130					135					140				
Val	Thr	Asn	Gly	Ser	Thr	Arg	Val	Thr	Glu	Val	Arg	Ala	Arg	Phe	Ala
145					150					155					160
Leu	Asp	Ala	Met	Pro	Gly	Lys	Gln	Met	Ala	Ile	Asp	Ala	Asp	Leu	Asn
			165					170						175	

Ser	Gly	Leu	Ile	Asp	Asp	Lys	Glu	Ala	Lys	Lys	Arg	Arg	Ala	Ala	Leu	180	185	190	
Ser	Gln	Glu	Ala	Asp	Phe	Tyr	Gly	Ala	Met	Asp	Gly	Ala	Ser	Lys	Phe	195	200	205	
Val	Lys	Gly	Asp	Ala	Ile	Ala	Ser	Ile	Ile	Ile	Thr	Leu	Ile	Asn	Ile	210	215	220	
Ile	Gly	Gly	Phe	Leu	Val	Gly	Val	Phe	Gln	Arg	Asp	Met	Ser	Leu	Ser	225	230	240	
Phe	Ser	Ala	Ser	Thr	Phe	Thr	Ile	Leu	Thr	Ile	Gly	Asp	Gly	Leu	Val	245	250	255	
Gly	Gln	Ile	Pro	Ala	Leu	Ile	Ile	Ala	Thr	Arg	Thr	Gly	Ile	Val	Ala	260	265	270	
Thr	Arg	Thr	Thr	Gln	Asn	Glu	Glu	Glu	Asp	Phe	Ala	Ser	Lys	Leu	Ile	275	280	285	
Thr	Gln	Leu	Thr	Asn	Lys	Ser	Lys	Thr	Leu	Val	Ile	Val	Gly	Ala	Ile	290	295	300	
Tyr	Cys	Phe	Cys	Thr	Ile	Pro	Gly	Leu	Pro	Thr	Phe	Ser	Leu	Ala	Phe	305	310	315	320
Val	Gly	Ala	Leu	Phe	Leu	Phe	Ile	Ala	Trp	Leu	Ile	Ser	Arg	Glu	Gly	325	330	335	
Lys	Asp	Gly	Leu	Leu	Thr	Lys	Leu	Glu	Asn	Tyr	Leu	Ser	Gln	Lys	Phe	340	345	350	
Gly	Leu	Asp	Leu	Ser	Glu	Lys	Pro	His	Ser	Ser	Lys	Ile	Lys	Pro	His	355	360	365	
Ala	Pro	Thr	Thr	Arg	Ala	Lys	Thr	Gln	Glu	Glu	Ile	Lys	Arg	Glu	Glu	370	375	380	
Glu	Gln	Ala	Ile	Asp	Glu	Val	Leu	Lys	Ile	Glu	Phe	Leu	Glu	Leu	Ala	385	390	395	400
Leu	Gly	Tyr	Gln	Leu	Tyr	Ser	Leu	Ala	Asp	Met	Lys	Gln	Gly	Gly	Asp	405	410	415	
Leu	Leu	Glu	Arg	Ile	Arg	Gly	Ile	Arg	Lys	Lys	Ile	Ala	Ser	Asp	Tyr	420	425	430	

Gly Phe Leu Met Pro Gln Ile Arg Ile Arg Asp Asn Leu Gln Leu Pro
 435 440 445
 Pro Thr His Tyr Glu Ile Lys Leu Lys Gly Ile Val Ile Gly Glu Gly
 450 455 460
 Met Val Met Pro Asp Lys Phe Leu Ala Met Asn Thr Gly Phe Val Asn
 465 470 475 480
 Lys Glu Ile Glu Gly Ile Pro Thr Lys Glu Pro Ala Phe Gly Met Asp
 485 490 495
 Ala Leu Trp Ile Glu Thr Lys Asn Lys Glu Glu Ala Ile Ile Gln Gly
 500 505 510
 Tyr Thr Ile Ile Asp Pro Ser Thr Val Ile Ala Thr His Thr Ser Glu
 515 520 525
 Leu Val Lys Lys Tyr Ala Glu Asp Phe Ile Thr Lys Asp Glu Val Lys
 530 535 540
 Ser Leu Leu Glu Arg Leu Ala Lys Asp Tyr Pro Thr Ile Val Glu Glu
 545 550 555 560
 Ser Lys Lys Ile Pro Thr Gly Ala Ile Arg Ser Val Leu Gln Ala Leu
 565 570 575
 Leu His Glu Lys Ile Pro Ile Lys Asp Met Leu Thr Ile Leu Glu Thr
 580 585 590
 Ile Thr Asp Ile Ala Pro Leu Val Gln Asn Asp Val Asn Ile Leu Thr
 595 600 605
 Glu Gln Val Arg Ala Arg Leu Ser Arg Val Ile Thr Asn Ala Phe Lys
 610 615 620
 Ser Glu Asp Gly Arg Leu Lys Phe Leu Thr Phe Ser Thr Asp Ser Glu
 625 630 635 640
 Gln Phe Leu Leu Asn Lys Leu Arg Glu Asn Gly Thr Ser Lys Ser Leu
 645 650 655
 Leu Leu Asn Val Gly Glu Leu Gln Lys Leu Ile Glu Ala Val Ser Glu
 660 665 670
 Glu Ala Met Lys Val Leu Gln Lys Gly Ile Ala Pro Val Ile Leu Ile
 675 680 685

Val Glu Pro Asn Leu Arg Lys Ala Leu Ser Asn Gln Met Glu Gln Ala
690 695 700

Arg Ile Asp Val Ile Val Leu Ser His Ala Glu Leu Asp Pro Asn Ser
705 710 715 720

Asn Phe Glu Ala Leu Gly Thr Ile His Ile Asn Phe
725 730

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 724 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Ala	Lys	Asn	Lys	Ile	Val	Asp	Leu	Val	Phe	Pro	Phe	Leu	Gly	Pro
1				5					10					15	
Leu	Ile	Ala	Pro	Val	Leu	Lys	Ala	Lys	Ser	Leu	Thr	Ile	Val	Gly	Phe
			20					25					30		
Leu	Val	Cys	Ile	Leu	Ala	Ile	Ile	Ile	Val	Pro	Leu	Pro	Ser	Pro	Ile
		35					40					45			
Leu	Asp	Phe	Phe	Leu	Ala	Leu	Ser	Ile	Ala	Leu	Ser	Val	Leu	Ile	Ile
	50					55					60				
Leu	Ile	Ser	Ile	Tyr	Ile	Pro	Lys	Pro	Thr	Asp	Leu	Thr	Thr	Phe	Pro
65					70					75					80
Thr	Leu	Ile	Leu	Ile	Ile	Thr	Leu	Phe	Arg	Leu	Ser	Leu	Asn	Ile	Ala
			85						90					95	
Thr	Thr	Arg	Met	Ile	Leu	Ser	Glu	Gly	Gln	Asn	Gly	Pro	Glu	Ala	Val
			100					105					110		
Ser	Glu	Ile	Ile	Ala	Ala	Phe	Gly	Glu	Phe	Val	Val	Gly	Gly	Asn	Met
		115					120					125			
Val	Ile	Gly	Val	Ile	Val	Phe	Cys	Ile	Leu	Val	Leu	Ile	Asn	Phe	Met
	130					135					140				
Val	Val	Thr	Lys	Gly	Ser	Thr	Arg	Val	Ser	Glu	Val	Gln	Ala	Arg	Phe
145					150					155					160
Thr	Leu	Asp	Ala	Met	Pro	Gly	Lys	Gln	Met	Ala	Ile	Asp	Ala	Asp	Leu
				165					170					175	

Asn Ala Gly Leu Ile Asp Glu Gln Thr Ala Arg Ala Arg Arg Gln Glu
 180 185 190
 Val Ile Ala Glu Ala Asn Phe Tyr Gly Ala Met Asp Gly Ser Ser Lys
 195 200 205
 Phe Ile Lys Gly Asp Ala Val Ala Gly Ile Ile Ile Thr Ile Ile Asn
 210 215 220
 Ile Ile Gly Gly Phe Leu Ile Gly Ser Phe Gln His Asp Met Ala Leu
 225 230 235 240
 Ser Asp Ala Ala Ser Thr Tyr Thr Ile Leu Thr Ile Gly Asp Gly Leu
 245 250 255
 Val Ser Gln Ile Pro Gly Leu Ile Thr Ser Thr Ala Thr Ala Ile Ile
 260 265 270
 Ile Thr Arg Ala Ser Lys Asp Glu Glu Asn Phe Ala Glu Gly Thr Leu
 275 280 285
 Thr Gln Leu Leu Ser Glu Tyr Arg Thr Leu Leu Ile Val Gly Phe Val
 290 295 300
 Leu Phe Ile Phe Ala Leu Val Pro Gly Leu Pro Thr Leu Ser Leu Gly
 305 310 315 320
 Phe Met Ala Leu Val Phe Leu Ser Leu Gly Tyr Leu Tyr Lys Gln Val
 325 330 335
 Lys Glu Gly Lys Ile Asp Ile Thr Thr Val Lys Lys Ser Lys Pro Ser
 340 345 350
 Ala Ala Val Ala Ser Gln Ser Gly Ala Gly Gly Thr Thr Ala Ala Pro
 355 360 365
 Ala Lys Lys Ser Glu Glu Glu Ile Leu Lys Glu Glu Glu His Lys Ile
 370 375 380
 Asn Asp Ile Leu Lys Val Glu Ile Leu Glu Leu Glu Leu Gly Tyr Gly
 385 390 395 400
 Leu Ile Lys Leu Ala Glu Asn Glu Leu Thr Glu Arg Ile Arg Ser Met
 405 410 415
 Arg Arg Ser Ile Ala Glu Ser Leu Gly Phe Leu Met Pro Lys Ile Arg
 420 425 430

Ile	Arg	Asp	Asn	Leu	Arg	Leu	Lys	Pro	Asn	Glu	Tyr	Ser	Phe	Lys	Leu	435	440	445	
Lys	Gly	Val	Ser	Ile	Ala	Ser	Ala	Glu	Ile	Tyr	Pro	Asp	Lys	Tyr	Leu	450	455	460	
Ala	Met	Asp	Ser	Gly	Phe	Ile	Thr	Glu	Glu	Ile	Glu	Gly	Ile	Ala	Thr	465	470	475	480
Lys	Glu	Pro	Ala	Phe	Asn	Ser	Asp	Ala	Leu	Trp	Ile	Asp	Ala	Asn	Leu	485	490	495	
Lys	Asp	Glu	Ala	Thr	Leu	Asn	Gly	Tyr	Ile	Val	Ile	Asp	Pro	Ala	Ser	500	505	510	
Val	Ile	Ser	Thr	His	Met	Ser	Glu	Leu	Ala	Lys	Ala	His	Ala	Ser	Glu	515	520	525	
Leu	Leu	Thr	Arg	Gln	Glu	Val	Gln	Asn	Leu	Leu	Asp	Lys	Val	Lys	Asn	530	535	540	
Asp	Tyr	Pro	Ile	Ile	Val	Glu	Gly	Ala	Leu	Gly	Val	Ala	Pro	Val	Ser	545	550	555	560
Leu	Ile	Gln	Lys	Ile	Leu	Lys	Asp	Leu	Leu	Lys	His	His	Ile	Pro	Ile	565	570	575	
Lys	Asp	Met	Leu	Thr	Ile	Leu	Glu	Ser	Val	Ser	Asp	Ile	Ala	Glu	Val	580	585	590	
Ser	Lys	Ser	Phe	Asp	Met	Ile	Ile	Glu	His	Val	Arg	Ala	Ser	Leu	Ala	595	600	605	
Arg	Met	Ile	Thr	Asn	Met	Tyr	Leu	Asp	Asp	Lys	Gly	Asn	Leu	Asp	Ile	610	615	620	
Phe	Ile	Leu	Asp	Ser	Ala	Ser	Ser	Ala	Val	Leu	Met	Glu	Asn	Val	Gln	625	630	635	640
Phe	Arg	Asp	Gly	Ser	Tyr	His	Leu	Pro	Leu	Ser	Val	Ala	Gln	Thr	Gly	645	650	655	
Thr	Leu	Val	Asp	Thr	Leu	Arg	Ala	Glu	Val	Ala	Ala	Val	Ala	Asn	Gly	660	665	670	
Arg	Ile	Lys	Pro	Phe	Ile	Leu	Cys	Val	Glu	Pro	Gln	Leu	Arg	Lys	Phe	675	680	685	

Ile Ala Asp Ile Cys Tyr Asn Phe Ser Ile Asn Ile Val Val Leu Ser
690 695 700

Phe Ala Glu Ile Ala Glu Asn Thr Asn Phe Asn Thr Glu Gly Ile Ile
705 710 715 720

Arg Ile Glu Leu

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 700 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Met	Ala	Asp	Ala	Ala	Ala	Pro	Asn	Ala	Ser	Ser	Met	Pro	Ser	Ala	Lys
1				5					10					15	
Ser	Leu	Leu	Asp	Gly	Leu	Met	Arg	Gly	Glu	Met	Gly	Leu	Ala	Leu	Gly
			20					25					30		
Val	Val	Gly	Ile	Ile	Val	Leu	Leu	Ile	Ile	Pro	Val	Pro	Ala	Pro	Leu
		35					40					45			
Leu	Asp	Val	Leu	Leu	Ala	Ile	Ser	Leu	Thr	Gly	Ser	Val	Leu	Ile	Leu
	50					55					60				
Met	Thr	Ala	Ile	Leu	Ile	Lys	Lys	Pro	Leu	Glu	Phe	Thr	Ser	Phe	Pro
65					70					75				80	
Thr	Val	Leu	Leu	Val	Thr	Thr	Leu	Phe	Arg	Leu	Gly	Leu	Asn	Ile	Ala
			85						90					95	
Ser	Thr	Arg	Leu	Ile	Leu	Ser	His	Gly	Gln	Glu	Gly	Thr	Gly	Gly	Ala
			100					105					110		
Gly	Ala	Val	Ile	Glu	Ala	Phe	Gly	His	Leu	Met	Met	Gln	Gly	Asn	Phe
		115					120					125			
Val	Ile	Gly	Val	Ile	Val	Phe	Ile	Ile	Leu	Ile	Val	Val	Asn	Phe	Met
	130					135					140				
Val	Val	Thr	Lys	Gly	Ser	Gly	Arg	Ile	Ala	Glu	Val	Ala	Ala	Arg	Phe
145					150					155				160	
Thr	Leu	Asp	Ser	Met	Pro	Gly	Lys	Gln	Met	Ala	Ile	Asp	Ala	Asp	Leu
				165					170					175	

Ser Thr Gly Leu Ile Ser Gln Asp Glu Ala Lys Ile Arg Arg Lys Glu
 180 185 190
 Leu Glu Gln Glu Ser Thr Phe Phe Gly Ala Met Asp Gly Ala Ser Lys
 195 200 205
 Phe Val Lys Gly Asp Ala Ile Ala Gly Leu Ile Ile Thr Ala Ile Asn
 210 215 220
 Ile Ile Gly Gly Ile Ile Ile Gly Val Val Gln His Lys Met Pro Phe
 225 230 235 240
 Gly Asp Ala Ala Ser Thr Tyr Thr Ile Met Thr Ile Gly Asp Gly Leu
 245 250 255
 Val Ser Gln Ile Pro Ala Leu Ile Ile Ser Ile Ala Ala Gly Met Val
 260 265 270
 Val Ser Lys Ala Gly Val Glu Gly Ser Ala Asp Lys Ala Leu Thr Thr
 275 280 285
 Gln Leu Ala Met Asn Pro Val Gly Leu Gly Met Val Ser Ala Ser Ser
 290 295 300
 Gly Ile Ile Ala Leu Ile Pro Gly Met Pro Ile Phe Pro Phe Ala Ala
 305 310 315 320
 Met Ala Leu Ala Ala Gly Ala Leu Ala Tyr Lys Arg Val Gln Asp Ala
 325 330 335
 Lys Lys Pro Lys Ala Leu Asp Pro Ala Asp Leu Glu Ala Ala Ala Pro
 340 345 350
 Ser Glu Pro Glu Glu Glu Pro Ile Ser Ala Ser Leu Ala Ile Asp Asp
 355 360 365
 Val Lys Ile Glu Leu Gly Tyr Gly Leu Leu Thr Leu Ile Asn Asp Leu
 370 375 380
 Asp Gly Arg Lys Leu Thr Asp Gln Ile Arg Ala Leu Arg Lys Thr Leu
 385 390 395 400
 Ala Ser Glu Tyr Gly Phe Val Met Pro Pro Val Arg Ile Leu Asp Asn
 405 410 415
 Met Arg Leu Ala Asn Gln Gly Tyr Ala Ile Arg Ile Lys Glu Met Glu
 420 425 430

Ala Gly Ala Gly Glu Val Arg Leu Gly Cys Leu Met Cys Met Asp Pro	435	440	445
Arg Gly Gly Gln Val Glu Leu Pro Gly Glu His Val Arg Glu Pro Ala	450	455	460
Phe Gly Leu Pro Ala Thr Trp Ile Ala Asp Asp Leu Arg Glu Glu Ala	465	470	475 480
Thr Phe Arg Gly Tyr Thr Val Val Asp Pro Ala Thr Val Leu Thr Thr	485	490	495
His Leu Thr Glu Ile Leu Lys Glu Asn Met Ala Asp Leu Leu Ser Tyr	500	505	510
Ala Glu Val Gln Lys Leu Leu Lys Glu Leu Pro Glu Thr Gln Lys Lys	515	520	525
Leu Val Asp Asp Leu Ile Pro Gly Thr Val Thr Ala Thr Thr Val Gln	530	535	540
Arg Val Leu Gln Ser Leu Leu Arg Glu Arg Val Ser Ile Arg Asp Leu	545	550	555 560
Pro Gln Ile Leu Glu Gly Val Gly Glu Ala Ala Pro His Thr Ala Ser	565	570	575
Val Thr Gln Leu Val Glu Gln Val Arg Ala Arg Leu Ala Arg Gln Leu	580	585	590
Cys Trp Ala Asn Arg Gly Asp Asp Gly Ala Leu Pro Ile Ile Thr Leu	595	600	605
Ser Ala Asp Trp Glu Gln Ala Phe Ala Glu Ala Leu Ile Gly Pro Gly	610	615	620
Asp Asp Lys Gln Leu Ala Leu Pro Pro Ser Arg Leu Gln Asp Phe Ile	625	630	635 640
Arg Gly Val Arg Asp Ser Phe Glu Arg Ala Ala Leu Ala Gly Glu Ala	645	650	655
Pro Val Leu Leu Thr Ser Pro Gly Val Arg Pro Tyr Val Arg Ser Ile	660	665	670
Ile Glu Arg Phe Arg Gly Gln Thr Val Val Met Ser Gln Asn Glu Ile	675	680	685
His Pro Arg Ala Arg Leu Lys Thr Val Gly Met Val	690	695	700

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 704 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met	Asn	Pro	His	Asp	Leu	Glu	Trp	Leu	Asn	Arg	Ile	Gly	Glu	Arg	Lys
1				5					10					15	
Asp	Ile	Met	Leu	Ala	Val	Leu	Leu	Leu	Ala	Val	Val	Phe	Met	Met	Val
		20						25					30		
Leu	Pro	Leu	Pro	Pro	Leu	Val	Leu	Asp	Ile	Leu	Ile	Ala	Val	Asn	Met
		35					40					45			
Thr	Ile	Ser	Val	Val	Leu	Leu	Met	Ile	Ala	Ile	Tyr	Ile	Asn	Ser	Pro
	50					55					60				
Leu	Gln	Phe	Ser	Ala	Phe	Pro	Ala	Val	Leu	Leu	Val	Thr	Thr	Leu	Phe
65				70						75				80	
Arg	Leu	Ala	Leu	Ser	Val	Ser	Thr	Thr	Arg	Met	Ile	Leu	Leu	Gln	Ala
			85						90					95	
Asp	Ala	Gly	Gln	Ile	Val	Tyr	Thr	Phe	Gly	Asn	Phe	Val	Val	Gly	Gly
		100						105					110		
Asn	Leu	Ile	Val	Gly	Ile	Val	Ile	Phe	Leu	Ile	Ile	Thr	Ile	Val	Gln
		115					120					125			
Phe	Leu	Val	Ile	Thr	Lys	Gly	Ser	Glu	Arg	Val	Ala	Glu	Val	Ser	Ala
	130					135					140				
Arg	Phe	Ser	Leu	Asp	Ala	Met	Pro	Gly	Lys	Gln	Met	Ser	Ile	Asp	Gly
145				150						155				160	
Asp	Met	Arg	Ala	Gly	Val	Ile	Asp	Val	Asn	Glu	Ala	Arg	Glu	Arg	Arg
			165					170					175		
Ala	Thr	Ile	Glu	Lys	Glu	Ser	Gln	Met	Phe	Gly	Ser	Met	Asp	Gly	Ala
		180					185						190		

Met Lys Phe Val Lys Gly Asp Ala Ile Ala Gly Leu Ile Ile Ile Phe
 195 200 205
 Val Asn Ile Leu Gly Gly Val Thr Ile Gly Val Thr Gln Lys Gly Leu
 210 215 220
 Ala Ala Ala Glu Ala Leu Gln Leu Tyr Ser Ile Leu Thr Val Gly Asp
 225 230 235 240
 Gly Met Val Ser Gln Val Pro Ala Leu Leu Ile Ala Ile Thr Ala Gly
 245 250 255
 Ile Ile Val Thr Arg Val Ser Ser Glu Asp Ser Ser Asp Leu Gly Ser
 260 265 270
 Asp Ile Gly Lys Gln Val Val Ala Gln Pro Lys Ala Met Leu Ile Gly
 275 280 285
 Gly Val Leu Leu Leu Leu Phe Gly Leu Ile Pro Gly Phe Pro Thr Val
 290 295 300
 Thr Phe Leu Ile Leu Ala Leu Leu Val Gly Cys Gly Gly Tyr Met Leu
 305 310 315 320
 Ser Arg Lys Gln Ser Arg Asn Asp Glu Ala Asn Gln Asp Leu Gln Ser
 325 330 335
 Ile Leu Thr Ser Gly Ser Gly Ala Pro Ala Ala Arg Thr Lys Ala Lys
 340 345 350
 Thr Ser Gly Ala Asn Lys Gly Arg Leu Gly Glu Gln Glu Ala Phe Ala
 355 360 365
 Met Thr Val Pro Leu Leu Ile Asp Val Asp Ser Ser Gln Gln Glu Ala
 370 375 380
 Leu Glu Ala Asn Ala Leu Asn Asp Glu Leu Val Arg Val Arg Arg Ala
 385 390 395 400
 Leu Tyr Leu Asp Leu Gly Val Pro Phe Pro Gly Ile His Leu Arg Phe
 405 410 415
 Asn Glu Gly Met Gly Glu Gly Glu Tyr Ile Ile Ser Leu Gln Glu Val
 420 425 430
 Pro Val Ala Arg Gly Glu Leu Lys Ala Gly Tyr Leu Leu Val Arg Glu
 435 440 445
 Ser Val Ser Gln Leu Glu Leu Leu Gly Ile Pro Tyr Glu Lys Gly Glu
 450 455 460

His	Leu	Leu	Pro	Asp	Gln	Glu	Ala	Phe	Trp	Val	Ser	Val	Glu	Tyr	Glu	465	470	475	480
Glu	Arg	Leu	Glu	Lys	Ser	Gln	Leu	Glu	Phe	Phe	Ser	His	Ser	Gln	Val	485	490	495	
Leu	Thr	Trp	His	Leu	Ser	His	Val	Leu	Arg	Glu	Tyr	Ala	Glu	Asp	Phe	500	505	510	
Ile	Gly	Ile	Gln	Glu	Thr	Arg	Tyr	Leu	Leu	Glu	Gln	Met	Glu	Gly	Gly	515	520	525	
Tyr	Gly	Glu	Leu	Ile	Lys	Glu	Val	Gln	Arg	Ile	Val	Pro	Leu	Gln	Arg	530	535	540	
Met	Thr	Glu	Ile	Leu	Gln	Arg	Leu	Val	Gly	Glu	Asp	Ile	Ser	Ile	Arg	545	550	555	560
Asn	Met	Arg	Ser	Ile	Leu	Glu	Ala	Met	Val	Glu	Trp	Gly	Gln	Lys	Glu	565	570	575	
Lys	Asp	Val	Val	Gln	Leu	Thr	Glu	Tyr	Ile	Arg	Ser	Ser	Leu	Lys	Arg	580	585	590	
Tyr	Ile	Cys	Tyr	Lys	Tyr	Ala	Asn	Gly	Asn	Asn	Ile	Leu	Pro	Ala	Tyr	595	600	605	
Leu	Phe	Asp	Gln	Glu	Val	Glu	Glu	Lys	Ile	Arg	Ser	Gly	Val	Arg	Gln	610	615	620	
Thr	Ser	Ala	Gly	Ser	Tyr	Leu	Ala	Leu	Glu	Pro	Ala	Val	Thr	Glu	Ser	625	630	635	640
Leu	Leu	Glu	Gln	Val	Arg	Lys	Thr	Ile	Gly	Asp	Leu	Ser	Gln	Ile	Gln	645	650	655	
Ser	Lys	Pro	Val	Leu	Ile	Val	Ser	Met	Asp	Ile	Arg	Arg	Tyr	Val	Arg	660	665	670	
Lys	Leu	Ile	Glu	Ser	Glu	Tyr	Tyr	Gly	Leu	Pro	Val	Leu	Ser	Tyr	Gln	675	680	685	
Glu	Leu	Thr	Gln	Gln	Ile	Asn	Ile	Gln	Pro	Leu	Gly	Arg	Ile	Cys	Leu	690	695	700	

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 685 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Met	Leu	Leu	Ser	Leu	Leu	Asn	Ser	Ala	Arg	Leu	Arg	Pro	Glu	Leu	Leu	
1				5					10					15		
Ile	Leu	Val	Leu	Met	Val	Met	Ile	Ile	Ser	Met	Phe	Val	Ile	Pro	Leu	
			20				25						30			
Pro	Thr	Tyr	Leu	Val	Asp	Phe	Leu	Ile	Ala	Leu	Asn	Ile	Val	Leu	Ala	
		35					40					45				
Ile	Leu	Val	Phe	Met	Gly	Ser	Phe	Tyr	Ile	Asp	Arg	Ile	Leu	Ser	Phe	
	50					55					60					
Ser	Thr	Phe	Pro	Ala	Val	Leu	Leu	Ile	Thr	Thr	Leu	Phe	Arg	Leu	Ala	
65					70					75					80	
Leu	Ser	Ile	Ser	Thr	Ser	Arg	Leu	Ile	Leu	Ile	Glu	Ala	Asp	Ala	Gly	
				85				90						95		
Glu	Ile	Ile	Ala	Thr	Phe	Gly	Gln	Phe	Val	Ile	Gly	Asp	Ser	Leu	Ala	
			100					105					110			
Val	Gly	Phe	Val	Val	Phe	Ser	Ile	Val	Thr	Val	Val	Gln	Phe	Ile	Val	
		115					120					125				
Ile	Thr	Lys	Gly	Ser	Glu	Arg	Val	Ala	Glu	Val	Ala	Ala	Arg	Phe	Ser	
	130					135					140					
Leu	Asp	Gly	Met	Pro	Gly	Lys	Gln	Met	Ser	Ile	Asp	Ala	Asp	Leu	Lys	
145						150				155					160	
Ala	Gly	Ile	Ile	Asp	Ala	Asp	Ala	Ala	Arg	Glu	Arg	Arg	Ser	Val	Leu	
				165					170						175	
Glu	Arg	Glu	Ser	Gln	Leu	Tyr	Gly	Ser	Phe	Asp	Gly	Ala	Met	Lys	Phe	
			180					185					190			

Ile Lys Gly Asp Ala Ile Ala Gly Ile Ile Ile Ile Phe Val Asn Phe
 195 200 205
 Ile Gly Gly Ile Ser Val Gly Met Thr Arg His Gly Met Asp Leu Ser
 210 215 220
 Ser Ala Leu Ser Thr Tyr Thr Met Leu Thr Ile Gly Asp Gly Leu Val
 225 230 235 240
 Ala Gln Ile Pro Ala Leu Leu Ile Ala Ile Ser Ala Gly Phe Ile Val
 245 250 255
 Thr Arg Val Asn Gly Asp Thr Asp Asn Met Gly Arg Asn Ile Met Thr
 260 265 270
 Gln Leu Leu Asn Asn Pro Phe Val Leu Val Val Thr Ala Ile Leu Thr
 275 280 285
 Ile Ser Met Gly Thr Leu Pro Gly Phe Pro Leu Pro Val Phe Val Ile
 290 295 300
 Leu Ser Val Val Leu Ser Val Leu Phe Tyr Phe Lys Phe Arg Glu Ala
 305 310 315 320
 Lys Arg Ser Ala Ala Lys Pro Lys Thr Ser Lys Gly Glu Gln Pro Leu
 325 330 335
 Ser Ile Glu Glu Lys Glu Gly Ser Ser Leu Gly Leu Ile Gly Asp Leu
 340 345 350
 Asp Lys Val Ser Thr Glu Thr Val Pro Leu Ile Leu Leu Val Pro Lys
 355 360 365
 Ser Arg Arg Glu Asp Leu Glu Lys Ala Gln Leu Ala Glu Arg Leu Arg
 370 375 380
 Ser Gln Phe Phe Ile Asp Tyr Gly Val Arg Leu Pro Glu Val Leu Leu
 385 390 395 400
 Arg Asp Gly Glu Gly Leu Asp Asp Asn Ser Ile Val Leu Leu Ile Asn
 405 410 415
 Glu Ile Arg Val Glu Gln Phe Thr Val Tyr Phe Asp Leu Met Arg Val
 420 425 430
 Val Asn Tyr Ser Asp Glu Val Val Ser Phe Gly Ile Asn Pro Thr Ile
 435 440 445
 His Gln Gln Gly Ser Ser Gln Tyr Phe Trp Val Thr His Glu Glu Gly
 450 455 460

Glu	Lys	Leu	Arg	Glu	Leu	Gly	Tyr	Val	Leu	Arg	Asn	Ala	Leu	Asp	Glu	465	470	475	480
Leu	Tyr	His	Cys	Leu	Ala	Val	Thr	Val	Ala	Arg	Asn	Val	Asn	Glu	Tyr	485	490	495	
Phe	Gly	Ile	Gln	Glu	Thr	Lys	His	Met	Leu	Asp	Gln	Leu	Glu	Ala	Lys	500	505	510	
Phe	Pro	Asp	Leu	Leu	Lys	Glu	Val	Leu	Arg	His	Ala	Thr	Val	Gln	Arg	515	520	525	
Ile	Ser	Glu	Val	Leu	Gln	Arg	Leu	Leu	Ser	Glu	Arg	Val	Ser	Val	Arg	530	535	540	
Asn	Met	Lys	Leu	Ile	Met	Glu	Ala	Leu	Ala	Leu	Trp	Ala	Pro	Arg	Glu	545	550	555	560
Lys	Asp	Val	Ile	Asn	Leu	Val	Glu	His	Ile	Arg	Gly	Ala	Met	Ala	Arg	565	570	575	
Tyr	Ile	Cys	His	Lys	Phe	Ala	Asn	Gly	Gly	Glu	Leu	Arg	Ala	Val	Met	580	585	590	
Val	Ser	Ala	Glu	Val	Glu	Asp	Val	Ile	Arg	Lys	Gly	Ile	Arg	Gln	Thr	595	600	605	
Ser	Gly	Ser	Thr	Phe	Leu	Ser	Leu	Asp	Pro	Glu	Ala	Ser	Ala	Asn	Leu	610	615	620	
Met	Asp	Leu	Ile	Thr	Leu	Lys	Leu	Asp	Asp	Leu	Leu	Ile	Ala	His	Lys	625	630	635	640
Asp	Leu	Val	Leu	Leu	Thr	Ser	Val	Asp	Val	Arg	Arg	Phe	Ile	Lys	Lys	645	650	655	
Met	Ile	Glu	Gly	Arg	Phe	Pro	Asp	Leu	Glu	Val	Leu	Ser	Phe	Gly	Glu	660	665	670	
Ile	Ala	Asp	Ser	Lys	Ser	Val	Asn	Val	Ile	Lys	Thr	Ile				675	680	685	

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 666 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

Met	Val	Met	Ile	Ile	Ala	Met	Leu	Ile	Ile	Pro	Leu	Pro	Thr	Tyr	Leu	
1				5					10					15		
Val	Asp	Phe	Leu	Ile	Gly	Leu	Asn	Ile	Val	Leu	Ala	Ile	Leu	Val	Phe	
			20					25					30			
Met	Gly	Ser	Phe	Tyr	Ile	Glu	Arg	Ile	Leu	Ser	Phe	Ser	Thr	Phe	Pro	
		35					40					45				
Ser	Val	Leu	Leu	Ile	Thr	Thr	Leu	Phe	Arg	Leu	Ala	Leu	Ser	Ile	Ser	
	50					55					60					
Thr	Ser	Arg	Leu	Ile	Leu	Val	Asp	Ala	Asp	Arg	Gly	Lys	Ile	Ile	Thr	
65				70						75					80	
Thr	Phe	Gly	Gln	Phe	Val	Ile	Gly	Asp	Ser	Leu	Ala	Val	Gly	Phe	Val	
			85					90						95		
Ile	Phe	Ser	Ile	Val	Thr	Val	Val	Gln	Phe	Ile	Val	Ile	Thr	Lys	Gly	
			100					105					110			
Ser	Glu	Arg	Val	Ala	Glu	Val	Ala	Ala	Arg	Phe	Ser	Leu	Asp	Gly	Met	
		115					120						125			
Pro	Gly	Lys	Gln	Met	Ser	Ile	Asp	Ala	Asp	Leu	Lys	Ala	Gly	Ile	Ile	
	130					135						140				
Asp	Ala	Ala	Gly	Ala	Lys	Glu	Arg	Arg	Ser	Ile	Leu	Glu	Arg	Glu	Ser	
145					150					155					160	
Gln	Leu	Tyr	Gly	Ser	Phe	Asp	Gly	Ala	Met	Lys	Phe	Ile	Lys	Gly	Asp	
			165						170					175		
Ala	Ile	Ala	Gly	Ile	Ile	Ile	Ile	Phe	Val	Asn	Leu	Ile	Gly	Gly	Ile	
			180					185						190		

Ser Val Gly Met Ser Gln His Gly Met Ser Leu Ser Gly Ala Leu Ser
 195 200 205
 Thr Tyr Thr Ile Leu Thr Ile Gly Asp Gly Leu Val Ser Gln Ile Pro
 210 215 220
 Ala Leu Leu Ile Ser Ile Ser Ala Gly Phe Met Leu Thr Arg Val Asn
 225 230 235 240
 Gly Asp Ser Asp Asn Met Gly Arg Asn Ile Met Ser Gln Ile Phe Gly
 245 250 255
 Asn Pro Phe Val Leu Ile Val Thr Ser Ala Leu Ala Leu Ala Ile Gly
 260 265 270
 Met Leu Pro Gly Phe Pro Phe Phe Val Phe Phe Leu Ile Ala Val Thr
 275 280 285
 Leu Thr Ala Leu Phe Tyr Tyr Lys Lys Val Val Glu Lys Glu Lys Ser
 290 295 300
 Leu Ser Glu Ser Asp Ser Ser Gly Tyr Thr Gly Thr Phe Asp Ile Asp
 305 310 315 320
 Asn Thr His Asp Ser Ser Leu Ala Met Ile Glu Asn Leu Asp Arg Ile
 325 330 335
 Ser Ser Glu Thr Val Pro Leu Ile Leu Leu Phe Ala Glu Asn Lys Ile
 340 345 350
 Asn Ala Asn Asp Met Glu Gly Leu Ile Glu Arg Ile Arg Ser Gln Phe
 355 360 365
 Phe Ile Asp Tyr Gly Val Arg Leu Pro Thr Ile Leu Tyr Arg Thr Ser
 370 375 380
 Asn Glu Leu Lys Val Asp Asp Ile Val Leu Leu Ile Asn Glu Val Arg
 385 390 395 400
 Ala Asp Ser Phe Asn Ile Tyr Phe Asp Lys Val Cys Ile Thr Asp Glu
 405 410 415
 Asn Gly Asp Ile Asp Ala Leu Gly Ile Pro Val Val Ser Thr Ser Tyr
 420 425 430
 Asn Glu Arg Val Ile Ser Trp Val Asp Val Ser Tyr Thr Glu Asn Leu
 435 440 445
 Thr Asn Ile Asp Ala Lys Ile Lys Ser Ala Gln Asp Glu Phe Tyr His
 450 455 460

Gln Leu Ser Gln Ala Leu Leu Asn Asn Ile Asn Glu Ile Phe Gly Ile
 465 470 475 480
 Gln Glu Thr Lys Asn Met Leu Asp Gln Phe Glu Asn Arg Tyr Pro Asp
 485 490 495
 Leu Leu Lys Glu Val Phe Arg His Val Thr Ile Gln Arg Ile Ser Glu
 500 505 510
 Val Leu Gln Arg Leu Leu Gly Glu Asn Ile Ser Val Arg Asn Leu Lys
 515 520 525
 Leu Ile Met Glu Ser Leu Ala Leu Trp Ala Pro Arg Glu Lys Asp Val
 530 535 540
 Ile Thr Leu Val Glu His Val Arg Ala Ser Leu Ser Arg Tyr Ile Cys
 545 550 555 560
 Ser Lys Ile Ala Val Ser Gly Glu Ile Lys Val Val Met Leu Ser Gly
 565 570 575
 Tyr Ile Glu Asp Ala Ile Arg Lys Gly Ile Arg Gln Thr Ser Gly Gly
 580 585 590
 Ser Phe Leu Asn Met Asp Ile Glu Val Ser Asp Glu Val Met Glu Thr
 595 600 605
 Leu Ala His Ala Leu Arg Glu Leu Arg Asn Ala Lys Lys Asn Phe Val
 610 615 620
 Leu Leu Val Ser Val Asp Ile Arg Arg Phe Val Lys Arg Leu Ile Asp
 625 630 635 640
 Asn Arg Phe Lys Ser Ile Leu Val Ile Ser Tyr Ala Glu Ile Asp Glu
 645 650 655
 Ala Tyr Thr Ile Asn Val Leu Lys Thr Ile
 660 665

C1
 cont